

3. Streszczenie w języku angielskim

Climate change as a serious threat to world food security. The current weather conditions are a factor that has a significant impact on the infestation of maize grain by fungi of the genus *Fusarium* spp. In view of the above, the aim of the dissertation was a multifaceted analysis of the genetic mechanisms involved in maize resistance to fungi of the genus *Fusarium* spp. causing fusariosis of maize cobs. As a result of the analyses, through the use of next-generation sequencing and association mapping, new molecular markers, coupled to candidate genes, were identified that were associated with resistance to fungi from genus *Fusarium* spp. in maize. From identified molecular markers, 26 were selected (significant at the 0.001 level) and converted to specific markers. Optimization of reaction conditions allowed, to identify silcoDArT markers (553, 13242, 11801, 24753) and SNPs (58153), which differentiated between reference genotypes susceptible and resistant to *Fusarium* spp. infection. In view of the foregoing, they can be used in breeding programs to select resistant genotypes, due to reducing the time required to breed new varieties. Based on physical mapping, eight of 26 relevant molecular markers were found to be located inside the genes. The location of markers within genes and their characterization in literature reports allowed the selection of four markers (553, 15097, 58771, 27775) that are conjugated to potential candidate genes (*GDSL esterase/lipase gene At4g01130 precursor uncharacterized precursor of the protein, putrescine hydroxycinnamyltransferase gene, peroxidase precursor gene 72 and pentatricopeptide repeat-containing protein At5g57250, mitochondrial*). Expression analysis of four candidate genes showed that they were characterized by elevated expression levels after inoculation, indicating their participation in the resistance response to infection by *Fusarium* spp. The peroxidase 72 precursor was characterized by the highest level of expression after inoculation in all genotypes tested, which may predispose it, to a gene potentially carrying resistance to *Fusarium* spp. Genotypes from the same breeding company showed similar expression patterns, suggesting that they may differ in origin. As a result, *beta tubulin* (β -TUB) and *cyclophilin* (CYP) were selected as reference genes for RT-qPCR analyses. Identification of fungi of the genus *Fusarium* spp. that were present on infested maize kernels made it possible to determine that the most abundant fungi occurred *Fusarium poae*, and single samples were also populated by *Fusarium ploriferatum* or *Fusarium culmorum*.

Key words: maize, *Fusarium*, MAS, NGS, silcoDArT